



RAW SEQUENCE LISTING ERROR REPORT

1652

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/697,186
Source: 1600
Date Processed by STIC: 2/22/2002

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MAR 1 2 2002
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/697,186</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

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**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/697,186**

DATE: 02/22/2002
TIME: 14:56:40

Input Set: I697186.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

1 <110> RIKEN
2 <120> A MUTANT KANAMYCIN NUCLEOTIDYLTRANSFERASE AND A METHOD OF SCREENING
3 THERMOPHILIC BACTERIA USING THE SAME
4 <130> PH-1082
5 <140> US/09/697,186
6 <141> 2000-10-27
7 <150> JP 11-309616
8 <151> 29-OCT-1999
9 <160> 11
10 <170> PatentIn Ver. 2.0

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pp 1-5

ERRORED SEQUENCES FOLLOW

11 <210> 1
12 <211> 253
13 <212> PRT
14 <213> Artificial Sequence
15 <220>
16 <223> mutantenzyme obtained by introduction of point mutation into wild type KNT
17 gene of *Staphylococcus aureus* and its expression
18 <400> 1
19 Met Asn Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile Val
20 1 5 10 15 misaligned
21 His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val Lys amino
22 20 25 30 acid
23 Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro Tyr
24 35 40 45 number
25 Ser Asp Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu Phe
26 50 55 60 (see item 3
27 Ser His Glu Trp Thr Thr Gly Glu Trp Lys Val Glu Val Asn Phe Tyr
28 65 70 75 on Error
29 Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp Trp
30 85 90 95 Summary
31 Pro Leu Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp Ser
32 100 105 110 Sheet)
33 Gly Gly Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu Ala
34 115 120 125
35 Gln Lys Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu Phe
36 130 135 140
37 Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr Thr
38 145 150 155 160
39 Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met Leu

Input Set: I697186.RAW

```

40                               165                               170                               175
41 Ile Gly Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val Leu
42                               180                               185                               190
43 Thr Glu Ala Val Lys Gln Ser Asp Leu Pro Ser Gly Tyr Asp His Leu
44                               195                               200                               205
45 Cys Gln Phe Val Met Ser Gly Gln Leu Ser Asp Ser Glu Lys Leu Leu
46                               210                               215                               220
47 Glu Ser Leu Glu Asn Phe Trp Asn Gly Ile Gln Glu Trp Thr Glu Arg
48                               225                               230                               235                               240
49 His Gly Tyr Ile Val Asp Val Ser Lys Arg Ile Pro Phe
50                               245                               250

```

51 <210> 3
52 <211> 253
53 <212> PRT
54 <213> Artificial@Sequence
55 <220>
56 <223> mutant@enzyme@obtained@by@introduction@of@point mutation into wild
57 type KNT@gene of Staphylococcus aureus and its@expression
58 <400> 3
59 Met Lys Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile Val
60 1 5 10 15
61 His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val Lys
62 20 25 30
63 Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro Tyr
64 35 40 45
65 Ser Asp Ile Glu Met Met Cys Val Leu Ser Thr Glu Gly Val Glu Phe
66 50 55 @@@@ @@@@ 60 misaligned nos.
67 Ser Tyr Glu Trp Thr Thr Gly Glu Trp Lys Ala Glu Val Asn Phe Tyr
68 65 70 75 80
69 Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Arg Val Glu Pro Asp Trp
70 85 90 95
71 Pro Leu Thr His Gly Arg Phe Phe Ser Ile Leu Pro Ile Tyr Asp Pro
72 100 105 110
73 Gly Gly Tyr Phe Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu Ala
74 115 120 125
75 Gln Lys Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu Phe
76 130 135 140
77 Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr Thr
78 145 150 155 160
79 Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met Leu
80 165 170 175
81 Ile Gly Leu His His Arg Ile Cys Tyr Thr Ser Ala Ser Val Leu
82 180 185 190
83 Thr Glu Ala Val Lys Gln Pro Asp Leu Pro Pro Gly Tyr Val Gln Leu
84 195 200 205
85 Cys Gln Leu Val Met Ser Gly Gln Leu Ser Asp Pro Glu Lys Leu Leu
86 210 215 220
87 Glu Ser Leu Glu Asn Phe Trp Asn Gly Val Gln Glu Trp Ala Glu Arg
88 225 230 235 240

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/697,186DATE: 02/22/2002
TIME: 14:56:40

Input Set: I697186.RAW

89	His Gly Tyr Ile Val Asp Val Ser Lys Arg Ile Pro Phe
90	245 250

91 <210> 10
 E--> 92 <211> 759
 93 <212> DNA
 94 <213> Staphylococcus aureus
 95 <220>
 96 <221> CDS
 97 <222> (1)..(759)
 98 <400> 10

99 gtg aat gga cca ata ata atg act aga gaa gaa aga atg aag att gtt 48 Met

W--> 100 Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile
 101 1 5 10 15

W--> 102 cat gaa att aag gaa cga ata ttg gat aaa tat ggg gat gat gtt aag 96 His

W--> 103 Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val
 104 20 25 30

W--> 105 gct att ggt gtt tat ggc tct ctt ggt cgt cag act gat ggg ccc tat 144 Ala

E--> 106 Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro
 107 35 40 45

W--> 108 tcg gat att gag atg atg tgt gtc atg tca aca gag gaa gca gag ttc 192 Ser

W--> 109 Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu
 110 50 55 60

E--> 111 agc cat gaa tgg aca acc ggt gag tgg aag gtg gaa gtg aat ttt gat 240 Ser

W--> 112 Glu Trp Thr Thr Gly Glu Trp Lys Val Glu Val Asn Phe
 113 65 70 75 80

E--> 114 agc gaa gag att cta cta gat tat gca tct cag gtg gaa tca gat tgg 288 Ser

W--> 115 Glu Ile Leu Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp
 116 85 90 95

E--> 117 ccg ctt aca cat ggt caa ttt ttc tct att ttg ccg att tat gat tca 336 Pro

W--> 118 Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp
 119 100 105 110

E--> 120 ggt gga tac tta gag aaa gtg tat caa act gct aaa tcg gta gaa gcc 384 Gly

W--> 121 Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu
 122 115 120 125

E--> 123 caa acg ttc cac gat gcg att tgt gcc ctt atc gta gaa gag ctg ttt 432 Gln

W--> 124 Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu
 125 130 135 140

E--> 126 gaa tat gca ggc aaa tgg cgt aat att cgt gtg caa gga ccg aca aca 480 Glu

W--> 127 Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/697,186DATE: 02/22/2002
TIME: 14:56:40

Input Set: I697186.RAW

W--> 138	145	150	155	160	
E--> 139	ttt cta cca tcc ttg act gta cag gta gca atg gca ggt gcc atg ttg				528 Phe
W--> 140					
141	Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met				
W--> 142	165	170	175		
E--> 143	att ggt ctg cat cat cgc atc tgt tat acg acg agc gct tcg gtc tta				576 Ile
W--> 144					
145	Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val				
146	180	185	190		
E--> 147	act gaa gca gtt aag caa tca gat ctt cct tca ggt tat gac cat ctg				624 Thr
W--> 148					
149	Ala Val Lys Gln Ser Asp Leu Pro Ser Gly Tyr Asp His				
150	195	200	205		
E--> 151	tgc cag ttc gta atg tct ggt caa ctt tcc gac tct gag aaa ctt ctg				672 Cys
W--> 152					
153	Phe Val Met Ser Gly Gln Leu Ser Asp Ser Glu Lys Leu				
154	210	215	220		
E--> 155	gaa tcg cta gag aat ttc tgg aat ggg att cag gag tgg aca gaa cga				720 Glu
W--> 156					
157	Leu Glu Asn Phe Trp Asn Gly Ile Gln Glu Trp Thr Glu				
W--> 158	225	230	235	240	
E--> 159	cac gga tat ata gtg gat gtg tca aaa cgc ata cca ttt				759 His
W--> 160					
161	Tyr Ile Val Asp Val Ser Lys Arg Ile Pro				
W--> 162	245	250			

163 <210> 11 ? Please ensure 253 amino acids are shown in this sequence.
 E--> 164 <211> 253 ? delete see P 5
 165 <212> PRT
 166 <213> Staphylococcus aureus
 167 <400> 11
 168 Met Asn Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile
 169 1 5 10 15
 170 His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val
 171 20 25 30
 172 Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro
 173 35 40 45
 174 Ser Asp Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu
 175 50 55 60
 176 Ser His Glu Trp Thr Thr Gly Glu Trp Lys Val Glu Val Asn Phe
 177 65 70 75 80 misaligned
 178 Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp
 179 85 90 95
 180 Pro Leu Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp
 181 100 105 110
 182 Gly Gly Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu
 183 115 120 125
 184 Gln Thr Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu
 185 130 135 140
 186 Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr

NOS,

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/697,186DATE: 02/22/2002
TIME: 14:56:40

Input Set: I697186.RAW

187	145	150	155	160
188	Phe Leu Pro Ser Leu	Thr Val Gln Val	Ala Met Ala Gly Ala Met	
189	165	170	175	
190	Ile Gly Leu His His Arg	Ile Cys Tyr Thr Thr Ser Ala Ser Val		
191	180	185	190	
192	Thr Glu Ala Val Lys Gln Ser Asp	Leu Pro Ser Gly Tyr Asp His		
193	195	200	205	
194	Cys Gln Phe Val Met Ser Gly Gln	Leu Ser Asp Ser Glu Lys Leu		
195	210	215	220	
196	Glu Ser Leu Glu Asn Phe	Trp Asn Gly Ile Gln Glu Trp Thr Gly		
197	225	230	235	240
198	His Gly Tyr Ile Val Asp Val Ser Lys Arg	Ile Pro		
199	245	250		

E--> 200
E--> 201@@@
1/14

delete

*misaligned
nos.*

Input Set: I697186.RAW

Line ? Error/Warning

Original Text

107 E Wrong Amino Acid Designator
107 E Wrong Amino Acid Designator
107 E Wrong Amino Acid Designator

gct att ggt gtt tat ggc tct ctt ggt cgt c
gct att ggt gtt tat ggc tct ctt ggt cgt c
gct att ggt gtt tat ggc tct ctt ggt cgt c

Input Set: I697186.RAW

Line ? Error/Warning

Original Text

65

70

Input Set: I697186.RAW

Input Set: I697186.RAW

Line ? Error/Warning

Original Text

143 E Wrong Amino Acid Designator

att ggt ctg cat cat cgc atc tgt tat acg a

Input Set: I697186.RAW

Line ? Error/Warning

Original Text

Input Set: I697186.RAW

Line ? Error/Warning

Original Text

156 W Invalid/Missing Amino Acid Numbering
158 W Invalid/Missing Amino Acid Numbering
159 E Wrong Amino Acid Designator
160 W Invalid/Missing Amino Acid Numbering
162 W Invalid/Missing Amino Acid Numbering
164 E Input 253, Calc Seq.Length 254 differ
200 E Wrong Amino Acid Designator
201 E Invalid/Missing Amino Acid Numbering

225 230 2
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
cac gga tat ata gtg gat gtg tca aaa cgc a
245 250
<211> 253
@@@
1/14